

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/766,350A

1642

DATE: 07/14/98
TIME: 08:47:37

INPUT SET: S3230.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

Page #18

SEQUENCE LISTING

ENTERED

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Chatterjee, Malaya
6 Foon, Kenneth A.
7 Chatterjee, Sunil K.
8
9 (ii) TITLE OF INVENTION: MURINE MONOCLONAL ANTI-IDIOTYPE ANTIBODY
10 11D10 AND METHODS OF USE THEREOF
11
12 (iii) NUMBER OF SEQUENCES: 59
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: MORRISON & FOERSTER
16 (B) STREET: 755 PAGE MILL ROAD
17 (C) CITY: PALO ALTO
18 (D) STATE: CA
19 (E) COUNTRY: USA
20 (F) ZIP: 94304-1018
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER: US 08/766,350
30 (B) FILING DATE: 13-DEC-1996
31 (C) CLASSIFICATION:
32
33 (viii) ATTORNEY/AGENT INFORMATION:
34 (A) NAME: Polizzi, Catherine M.
35 (B) REGISTRATION NUMBER: 40,130
36 (C) REFERENCE/DOCKET NUMBER: 30414-20003.21
37
38 (ix) TELECOMMUNICATION INFORMATION:
39 (A) TELEPHONE: (650) 813-5600
40 (B) TELEFAX: (650) 494-0792
41 (C) TELEX: 706141
42
43
44 (2) INFORMATION FOR SEQ ID NO:1:
45
46 (i) SEQUENCE CHARACTERISTICS:

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47         (A) LENGTH: 435 base pairs
48         (B) TYPE: nucleic acid
49         (C) STRANDEDNESS: single
50         (D) TOPOLOGY: linear
51
52     (ii) MOLECULE TYPE: DNA (genomic)
53
54
55     (ix) FEATURE:
56         (A) NAME/KEY: CDS
57         (B) LOCATION: 1..435
58
59     (ix) FEATURE:
60         (A) NAME/KEY: mat_peptide
61         (B) LOCATION: 61
62
63
64     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
65
66     ATG GGG GCC CCT GCT CAG ATT CTT GGG TTC TTG TTG CTC TTG TTT CCA      48
67     Met Gly Ala Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Leu Phe Pro
68     -20                      -15                      -10                      -5
69
70     GGT ACC AGA TGT GAC ATC CAG ATG ACC CAG TCT CCA TCC TCC TTA TCT      96
71     Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
72                      1                      5                      10
73
74     GCC TCT CTG GGA CAA AGA GTC AGT CTC ACT TGT CGG GCA AGT CAG GAC      144
75     Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp
76     15                      20                      25
77
78     ATT GGT ATT AAC TTA CAT TGG CTT CAG CAG GAA CCA GAT GGA ACT ATT      192
79     Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile
80     30                      35                      40
81
82     AAA CGC CTG ATC TAC GCC ACA TCC AGT TTA GGT TCT GGT GTC CCC AAA      240
83     Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys
84     45                      50                      55                      60
85
86     AGG TTC AGT GGC AGT AGG TCT GGG TCA GAT TAT TCT CTC ACC ATC AGC      288
87     Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser
88                      65                      70                      75
89
90     AGC CTT GAG TCT GAA GAT TTT GTA GCC TAT TAC TGT CTA CAA TAT GCT      336
91     Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala
92     80                      85                      90
93
94     AGT TCT CCG TAC ACG TTC GGA GGG GGG ACC AAG CTG GAA ATA AAA CGG      384
95     Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
96     95                      100                      105
97
98     GCT GAT GCT GCA CCA ACT GTA TCC ATC TTC CCA CCA TCC AGT AAG CTT      432
99     Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu

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100      110      115      120
101
102      GGG
103      Gly
104      125
105
106
107      (2) INFORMATION FOR SEQ ID NO:2:
108
109          (i) SEQUENCE CHARACTERISTICS:
110              (A) LENGTH: 145 amino acids
111              (B) TYPE: amino acid
112              (D) TOPOLOGY: linear
113
114          (ii) MOLECULE TYPE: protein
115
116          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
117
118      Met Gly Ala Pro Ala Gln Ile Leu Gly Phe Leu Leu Leu Leu Phe Pro
119      -20      -15      -10      -5
120
121      Gly Thr Arg Cys Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser
122              1      5      10
123
124      Ala Ser Leu Gly Gln Arg Val Ser Leu Thr Cys Arg Ala Ser Gln Asp
125              15      20      25
126
127      Ile Gly Ile Asn Leu His Trp Leu Gln Gln Glu Pro Asp Gly Thr Ile
128              30      35      40
129
130      Lys Arg Leu Ile Tyr Ala Thr Ser Ser Leu Gly Ser Gly Val Pro Lys
131              45      50      55      60
132
133      Arg Phe Ser Gly Ser Arg Ser Gly Ser Asp Tyr Ser Leu Thr Ile Ser
134              65      70      75
135
136      Ser Leu Glu Ser Glu Asp Phe Val Ala Tyr Tyr Cys Leu Gln Tyr Ala
137              80      85      90
138
139      Ser Ser Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Arg
140              95      100      105
141
142      Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro Ser Ser Lys Leu
143              110      115      120
144
145      Gly
146      125
147
148      (2) INFORMATION FOR SEQ ID NO:3:
149
150          (i) SEQUENCE CHARACTERISTICS:
151              (A) LENGTH: 461 base pairs
152              (B) TYPE: nucleic acid

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153         (C) STRANDEDNESS: single
154         (D) TOPOLOGY: linear
155
156     (ii) MOLECULE TYPE: DNA (genomic)
157
158
159     (ix) FEATURE:
160         (A) NAME/KEY: CDS
161         (B) LOCATION: 1..459
162
163     (ix) FEATURE:
164         (A) NAME/KEY: mat_peptide
165         (B) LOCATION: 58
166
167
168     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
169
170     ATG GAA TGC AGC TGG GTC TTT CTC TTC CTC CTG TCA ATA ACT ACA GGT      48
171     Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly
172     -19                -15                -10                -5
173
174     GTC CAC TCC CAG GCT TAT CTA CAG CAG TCT GGG GCT GAG CTG GTG AGG      96
175     Val His Ser Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
176                1                5                10
177
178     TCT GGG GCC TCA GTG AAG ATG TCC TGC AAG GCT TCT GGC TAC ACA TTG      144
179     Ser Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu
180         15                20                25
181
182     ACC AGT TAC AAT ATG CAC TGG GTA AAG CAG ACA CCT GGA CAG GGC CTG      192
183     Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu
184         30                35                40                45
185
186     GAA TGG ATT GGA AAT ATT TTT CCT GGA AAT GGT GAT ACT TAC TAC AAT      240
187     Glu Trp Ile Gly Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn
188                50                55                60
189
190     CAG AAG TTT AAG GGC AAG GCC TCA TTG ACT GCA GAC ACA TCC TCC AGC      288
191     Gln Lys Phe Lys Gly Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser
192                65                70                75
193
194     ACA GCC TAC ATG CAG ATC AGC AGC CTG ACA TCT GAA GAC TCT GCG GTC      336
195     Thr Ala Tyr Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
196                80                85                90
197
198     TAT TTC TGT GCA AGA GGG AAC TGG GAG GGT GCT CTG GAC TAC TGG GGT      384
199     Tyr Phe Cys Ala Arg Gly Asn Trp Glu Gly Ala Leu Asp Tyr Trp Gly
200         95                100                105
201
202     CAA GGA ACC TCA GTC ACC GTC TCC TCA GCC AAA ACG ACA CCC CCA CCC      432
203     Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro
204     110                115                120                125
205

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461

206 GTC TAT CCA CTG GTC CCT GGA AGC TTG GG
207 Val Tyr Pro Leu Val Pro Gly Ser Leu
208 130
209
210

211 (2) INFORMATION FOR SEQ ID NO:4:
212

213 (i) SEQUENCE CHARACTERISTICS:
214 (A) LENGTH: 153 amino acids
215 (B) TYPE: amino acid
216 (D) TOPOLOGY: linear
217

218 (ii) MOLECULE TYPE: protein
219

220 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
221

222 Met Glu Cys Ser Trp Val Phe Leu Phe Leu Leu Ser Ile Thr Thr Gly
223 -19 -15 -10 -5
224

225 Val His Ser Gln Ala Tyr Leu Gln Gln Ser Gly Ala Glu Leu Val Arg
226 1 5 10
227

228 Ser Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Leu
229 15 20 25
230

231 Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu
232 30 35 40 45
233

234 Glu Trp Ile Gly Asn Ile Phe Pro Gly Asn Gly Asp Thr Tyr Tyr Asn
235 50 55 60
236

237 Gln Lys Phe Lys Gly Lys Ala Ser Leu Thr Ala Asp Thr Ser Ser Ser
238 65 70 75
239

240 Thr Ala Tyr Met Gln Ile Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
241 80 85 90
242

243 Tyr Phe Cys Ala Arg Gly Asn Trp Glu Gly Ala Leu Asp Tyr Trp Gly
244 95 100 105
245

246 Gln Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Pro
247 110 115 120 125
248

249 Val Tyr Pro Leu Val Pro Gly Ser Leu
250 130
251

252 (2) INFORMATION FOR SEQ ID NO:5:
253

254 (i) SEQUENCE CHARACTERISTICS:
255 (A) LENGTH: 321 base pairs
256 (B) TYPE: nucleic acid
257 (C) STRANDEDNESS: single
258 (D) TOPOLOGY: linear

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SEQUENCE VERIFICATION REPORT
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